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RAW SEQUENCE LISTING   DATE: 01/23/2002
PATENT APPLICATION: US/09/997,522   TIME: 10:04:02

Input Set : N:\Crf3\RULE60\09997522.raw.txt
Output Set: N:\CRF3\01232002\I997522.raw

SEQUENCE LISTING
```
  3 (1) GENERAL INFORMATION:
  5      (i) APPLICANT: Coleman, Roger
  6                    Au-Young, Janice
  7                    Bandman, Olga
  8                    Seilhamer, Jeffrey J.
 10     (ii) TITLE OF INVENTION: Thrombin Receptor Homolog
 12    (iii) NUMBER OF SEQUENCES: 2
 14     (iv) CORRESPONDENCE ADDRESS:
 15.         (A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 16          (B) STREET: 3330 Hillview Avenue
 17          (C) CITY: Palo Alto
 18          (D) STATE: CA
 19          (E) COUNTRY: USA
 20          (F) ZIP: 94304
 22      (v) COMPUTER READABLE FORM:
 23          (A) MEDIUM TYPE: Floppy disk
 24          (B) COMPUTER: IBM PC compatible
 25          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 26          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 28     (vi) CURRENT APPLICATION DATA:
 29          (A) APPLICATION NUMBER: US/09/997,522     C-->
 30          (B) FILING DATE: 28-Nov-2001              C-->
 31          (C) CLASSIFICATION:
 33    (vii) PRIOR APPLICATION DATA:
 34          (A) APPLICATION NUMBER: 08/467,125
 35          (B) FILING DATE:
 39   (viii) ATTORNEY/AGENT INFORMATION:
 40          (A) NAME: Luther, Barbara J.
 41          (B) REGISTRATION NUMBER: 33954
 42          (C) REFERENCE/DOCKET NUMBER: PF-0041 US
 44     (ix) TELECOMMUNICATION INFORMATION:
 45          (A) TELEPHONE: 415-855-0555
 46          (B) TELEFAX: 415-852-0195
 49 (2) INFORMATION FOR SEQ ID NO: 1:
 51      (i) SEQUENCE CHARACTERISTICS:
 52          (A) LENGTH: 1143 base pairs
 53          (B) TYPE: nucleic acid
 54          (C) STRANDEDNESS: single
 55          (D) TOPOLOGY: linear
 57     (ii) MOLECULE TYPE: cDNA
 60    (vii) IMMEDIATE SOURCE:
 61          (A) LIBRARY: Liver
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 62            (B) CLONE: 86700
 66      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 68 ATGAGAAGTC ATACCATAAC AATGACGACA ACTTCAGTCA GCAGCTGGCC TTACTCCTCC      60
 70 CACAGAATGC GCTTTATAAC CAATCATAGC GACCAACCGC CACAAAACTT CTCAGCAACA     120
 72 CCAAATGTTA CTACCTGTCC CATGGATGAA AAATTGCTAT CTACTGTGTT AACCACATCC     180
 74 TACTCTGTTA TTTTCATCGT GGGACTGGTT GGGAACATAA TCGCCCCCTA TGTATTTCTG     240
 76 GGTATTCACC GTAAAAGAAA TTCCATTCAA ATTTATCTAC TTAACGTAGC CATTGCAGAC     300
 78 CTCCTACTCA TCTTCTGCCT CCCTTTCCGA ATAATGTATC ATATTAACCA AAACAAGTGG     360
 80 ACACTAGGTG TGATTCTGTG CAAGGTTGTG GGAACACTGC TTTATATGAA CATGTACATT     420
 82 AGCATTATTT TGCTTGGATT CATCAGTTTG GATCGCTATA TAAAAATTAA TCGGTCTATA     480
 84 CAGCAACGGA AGGCAATAAC AACCAAACAA AGTATTTATG TCTGTTGTAT AGTATGGATG     540
 86 CTTGCTCTTG GTGGATTCCT AACTATGATT ATTTTAACAC TTAAGAAAGG AGGGCATAAT     600
 88 TCCACAATGT GTTTCCATTA CAGAGATAAG CATAACGCAA AAGGAGAAGC CATTTTTAAC     660
 90 TTCATTCTTG TGGTAATGTT CTGGCTAATT TTCTTACTAA TAATCCTTTC ATATATTAAG     720
 92 ATTGGGAAGA ATCTATTGAG GATTTCTAAA AGGAGGTCAA AATTTCCTAA TTCTGGTAAA     780
 94 TATGCCACTA CAGCTCGTAA CTCCTTTATT GTACTTATCA TTTTTACTAT ATGTGTGGGT     840
 96 CCCTATCATG CCTTTCGATT CATCTACATT TCTTCACAGC TAAATGTATC ATCTTGCTAC     900
 98 TGGAAAGAAA TTGTTCACAA AACCAATGAG ATCATGCTGG TTCTCTCATC TTTCAATAGT     960
100 TGGTTAGATC CAGTCATGTA TTTCCTGATG TCCAGTAACA TTCGCAAAAT AATGTGCCAA    1020
102 CTTCTTTTTA GACGATTTCA AGGTGAACCA AGTAGGAGTG AAAGCACTTC AGAATTTAAA    1080
104 CCAGGATACT CCCTGCATGA TACATCTGTG GCAGGGAAAA TACAGTCTAG TTCTGAAAGT    1140
106 ACT                                                                 1143
110 (2) INFORMATION FOR SEQ ID NO: 2:
112      (i) SEQUENCE CHARACTERISTICS:
113          (A) LENGTH: 381 amino acids
114          (B) TYPE: amino acid
115          (D) TOPOLOGY: linear
117      (ii) MOLECULE TYPE: protein
119      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
121 Met Arg Ser His Thr Ile Thr Met Thr Thr Thr Ser Val Ser Ser Trp
122  1               5                  10                  15
124 Pro Tyr Ser Ser His Arg Met Arg Phe Ile Thr Asn His Ser Asp Gln
125              20                  25                  30
127 Pro Pro Gln Asn Phe Ser Ala Thr Pro Asn Val Thr Thr Cys Pro Met
128              35                  40                  45
130 Asp Glu Lys Leu Leu Ser Thr Val Leu Thr Thr Ser Tyr Ser Val Ile
131         50                  55                  60
133 Phe Ile Val Gly Leu Val Gly Asn Ile Ile Ala Pro Tyr Val Phe Leu
134 65                  70                  75                  80
136 Gly Ile His Arg Lys Arg Asn Ser Ile Gln Ile Tyr Leu Leu Asn Val
137              85                  90                  95
139 Ala Ile Ala Asp Leu Leu Leu Ile Phe Cys Leu Pro Phe Arg Ile Met
140             100                 105                 110
142 Tyr His Ile Asn Gln Asn Lys Trp Thr Leu Gly Val Ile Leu Cys Lys
143             115                 120                 125
145 Val Val Gly Thr Leu Leu Tyr Met Asn Met Tyr Ile Ser Ile Ile Leu
146         130                 135                 140
148 Leu Gly Phe Ile Ser Leu Asp Arg Tyr Ile Lys Ile Asn Arg Ser Ile
149 145                 150                 155                 160
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151 Gln Gln Arg Lys Ala Ile Thr Thr Lys Gln Ser Ile Tyr Val Cys Cys
152             165             170             175
154 Ile Val Trp Met Leu Ala Leu Gly Gly Phe Leu Thr Met Ile Ile Leu
155             180             185             190
157 Thr Leu Lys Lys Gly Gly His Asn Ser Thr Met Cys Phe His Tyr Arg
158             195             200             205
160 Asp Lys His Asn Ala Lys Gly Glu Ala Ile Phe Asn Phe Ile Leu Val
161     210             215             220
163 Val Met Phe Trp Leu Ile Phe Leu Leu Ile Ile Leu Ser Tyr Ile Lys
164 225             230         .       235             240
166 Ile Gly Lys Asn Leu Leu Arg Ile Ser Lys Arg Arg Ser Lys Phe Pro
167             245             250             255
169 Asn Ser Gly Lys Tyr Ala Thr Thr Ala Arg Asn Ser Phe Ile Val Leu
170             260             265             270
172 Ile Ile Phe Thr Ile Cys Val Gly Pro Tyr His Ala Phe Arg Phe Ile
173             275             280             285
175 Tyr Ile Ser Ser Gln Leu Asn Val Ser Ser Cys Tyr Trp Lys Glu Ile
176     290             295             300
178 Val His Lys Thr Asn Glu Ile Met Leu Val Leu Ser Ser Phe Asn Ser
179 305             310             315             320
181 Trp Leu Asp Pro Val Met Tyr Phe Leu Met Ser Ser Asn Ile Arg Lys
182             325             330             335
184 Ile Met Cys Gln Leu Leu Phe Arg Arg Phe Gln Gly Glu Pro Ser Arg
185             340             345             350
187 Ser Glu Ser Thr Ser Glu Phe Lys Pro Gly Tyr Ser Leu His Asp Thr
188             355             360             365
191 Ser Val Ala Gly Lys Ile Gln Ser Ser Ser Glu Ser Thr
192     370             375             380
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/997,522**

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]